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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Holmes, Stephen D.

 Gross, Mitchell S.

 Sylvester, Daniel R.
- (ii) TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in Treatment of IL4 Mediated Disorders
- (iii) NUMBER OF SEQUENCES: 58
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SmithKline Beecham Corporation
 - (B) STREET: Corporate Intellectual Property, UW2220 709
 Swedeland Rd.
 - (C) CITY: King of Prussia
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19406-2799
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/117,366
 - (B) FILING DATE: 07-SEP-1993
 - (C) CLASSIFICATION:
 - (A) APPLICATION NUMBER: US 08/136,783
 - (B) FILING DATE: 14-OCT-1993
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Sutton, Jeffrey A.

- (B) REGISTRATION NUMBER: 34,028
- (C) REFERENCE/DOCKET NUMBER: P50186-2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (215) 270-5024
- (B) TELEFAX: (215) 270-5090

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: CDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	GAG	ACA	GAC	ACA	ATC	CTG	CTA	TGG	GTG	CTG	CTG	CTC	TGG	GTT	CCA	48	
Met	Glu	Thr	Asp	Thr	Ile	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro		
1				5					10				•	15			
GGC	TCC	ACT	GGT	GAC	ATT	GTG	CTG	ACC	CAA	TCT	CCA	GCT	TCT	TTG	GCT	96	
Gly	Ser	Thr	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala		
			20					25					30				
GTG	TCT	CTA	GGG	CAG	AGG	GCC	ACC	ATC	TCC	TGC	AAG	GCC	AGC	CAA	AGT	144	
Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ala	Ser	Gln	Ser		





WO 95/07301

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		•														
GTT	GAT	TAT	GAT	GGT	GAT	AGT	TAT	ATG	AAC	TGG	TAC	CAA	CAG	AAA	CCA	192
															Pro	
-	50					55				-	60					
								•								
GGA	CAG	CCA	CCC	AAA	CTC	CTC	ATC	TAT	GCT	GCA	TCC	AAT	CTA	GAA	TCT	240
						Leu										
65					70					75					80	
GGG	ATC	CCA	GCC	AGG	TTT	AGT	GGC	AGT	GGG	TCT	GGG	ACA	GAC	TTC	ACC	288
Giy	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	
				85					90					95		
CTC	AAC	ATC	CAT	CCT	GTG	GAG	GAG	GAG	GAT	GCT	GCA	ACC	TAT	TAC	TGT	336
Leu	Asn	Ile	His	Pro	Val	Glu	Glu	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	
			100					105					110			•
						CCT										384
Gln	Gln	Ser	Asn	Glu	Asp	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	
		115					120					125				
	,				-		•									
		AAA				•										396
		Lys	Arg													
	130															

- (2) INFORMATION FOR SEQ ID NO:2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro

1 5 10 15





Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala 20 25 30

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser 35 40 45

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 50 55 60

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser 65 70 75 80

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr 85 90 95

Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
100 105 110

Gin Gin Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu 115 120 125

Glu Ile Lys Arg 130

(2) INFORMATION FOR SEQ ID NO:3:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double .
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 64..483





(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAZ	ATTC	GCGG	CCG	CTAT	GCA (GGAC	CAATO	CA GO	CAGC	AGCAZ	A TG.	AGGA	AGTA	AGC	CTGTG	CA 60
GA	TATO	AAG	C AGO	G CT	r act	TCC	: TC#	A TTG	CTC	CTO	CTC	G AT	r GŤ	c cc	T GCA	108
	Met	: Ası	n Arç	Lei	Th:	Ser	Ser	Lev	Let	ı Let	l Le	u Ile	e Va	l Pri	o Ala	100
	1	L			5					10			, , ,		15	
																,
TAT	GIC	CTC	TCC	CAC	GTI	ACT	CTG	AAA	GAG	TCI	' GG	c cc	r GG(G AT	ATTG	156
Tyr	Val	. Le	ı Sei	G1r	Val	. Thr	Leu	Lys	Glu	Ser	Gly	Pro	Gly	, Ile	Leu	
				20					25				-	30		
CAG	ccc	TCC	CAG	ACC	CTC	AGT	CTG	ACT	TGT	' тст	ጥጥር	י דרים	r ccc	<u>-</u> •	TCA	204
Gln	Pro	Ser	Glr	Thr	Leu	Ser	Leu	Thr	Cvs	Ser	Phe	Ser	. GG	Dhe	Ser	204
			35	i				40					45		. Jer	
											•		1.			
CTG	AGC	ACT	TCI	GGT	ATG	GGT	GTG	AGC	TGG	ATT	CGI	CAG	CCT	י דרי	GGA	252
Leu	Ser	Thr	Ser	Gly	Met	Gly	Val	Ser	Trp	Ile	Aro	Glo	Pro	Ser	Gly	252
		50	ı				55		•			60			Oly	
AAG	GGT	CTG	GAG	TGG	CTG	GCA	CAC	. ATT	TAC	TGG	GAT	GAT	GAC	AAG	CGC	300
Lys	Gly	Leu	Glu	Trp	Leu	Ala	His	Ile	Tyr	Trp	Asp	Asp	Asp	Lys	Arg	
	65					70					75			•		
TAT	AAC	CCA	TCC	CTG	AAG	AGC	CGG	CTC	ACA	ATC	TCC	AAC	Cam	3.00	TCC	
Tyr	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Leu	Thr	Tle	Ser	Luc	GAI	ACC	TCC	348
80					85		•			90	562	цуs	ASP	Int	ser 95	
															. 33	
AGC	AAC	CAG	GTA	TTC	CTC	AAG	ATC	ACC	AGT	GTG	ĠAC	ACT	GCA	GAT	ACT	396
Ser	Asn	Gln	Val	Phe	Leu	Lys	Ile	Thr	Ser	Val	Asp	Thr	Ala	Asp	Thr	330
				100	,				105		-			110		
GCC	ACA	TAC	TAC	TGT	GCT	CGA	AGA	GAG	ACT	CTC	~~ <i>c</i>					
Ala	Thr	Tyr	Tyr	Cvs	Ala	Arg	Ara	Glu	The	77-1	710	TAC	TGG	TAC	TTC	444
		-	115	-		3	9	120	****	4 G T	Elle	17.E	125	TYT	, Lue	
													123			
GAT	GTC	TGG	GGC .	GCA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA				483
Asp	Val	Trp	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser				403

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PCT/US94/10308

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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Leu Ile Val Pro Ala Tyr

1 5 10 15

Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
20 25 30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu 35 40 45

Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
50 55 60

Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
65 70 75 80

Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser 85 90 95

Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala

Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp 115 120 125

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser

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(2) INFORMATION	FOR	SEO	ID	NO:5:
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(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: CDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GTG TTG CAG ACC CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT

Met Val Leu Gin Thr Gin Val Phe Ile Ser Leu Leu Leu Trp Ile Ser

1 5 10 15

GGT GCC TAC GGG Gly Ala Tyr Gly

60

(2) INFORMATION FOR SEQ ID NO:6:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser



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15

Gly Ala Tyr Gly

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs.

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..57

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

10

GTC CAC TCC

ū

Val His Ser

57

48

(2) INFORMATION FOR SEQ ID NO:8:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein





(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 10 1

Val His Ser

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WO 95/07301

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..423
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

														ATC Ile		48
1				5	٠				10					15	561	
														ATA		96
Gly	Ala	Tyr	Gly	Gln	Val	Thr	Leu	Lys	Glu	Ser	Gly	Pro	Gly	Ile	Leu	
			20					25					30			
CAG	ccc	TCC	CAG	ACC	CTC	AGT	CTG	ACT	TGT	TCT	TTC	TCT	GGG	TTT	TCA	144
Gln	Pro	Ser	Gln	Thr	Leu	Ser	Leu	Thr	Cys	Ser	Phe	Ser	Gly	Phe	Ser	•
		35					40					45				
CTG	AGC	ACT	TCT	GGT	ATG	GGT	GTG	AGC	TGG	ATT	CGT	CAG	ССТ	TCA	GGA	192
Leu	Ser	Thr	Ser	Gly	Met	Gly	Val	Ser	Trp	Ile	Arg	Gln	Pro	Ser	Gly	
	50					55					60					

AAG	GGT	CTG	GAG	TGG	CTG	GCA	CAC	ATT	TAC	TGG	GAT	GAT	GAC	AAG	CGC	240
												Asp				
65					70					75				-	80	
TAT	AAC	CCA	TCC	CTG	AAG	ACC	ccc	ርሞር	NC N	3 mc	maa	AAG				
																288
TYL	VOII	PIO	Ser		rys	ser	Arg	Leu		Ile	Ser	Lys	Asp	Thr	Ser	
				85	•				90					95		
AGC	AAC	CAG	GTA	TTC	CTC	AAG	ATC	ACC	AGT	GTG	GAC	ACT	GCA	GAT	ACT	336
Ser	Asn	Gln	Val	Phe	Leu	Lуз	Ile	Thr	Ser	Val	Asp	Thr	Ala	Asp	Thr	
	•		100	•				105		-			110	•		٠
GCC	ACA	TAC	TAC	TGT	GCT	CGA	AGA	GAG	ACT	GTG	TTC	TAC	TGG	TAC	TTC	384
												Tyr				
		115				_	120					125		-,-		
												123				
GAT	GTC	TGG	GGC	GCA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA				423
										Val						-23
	130	-	_		-	135					140					
										•	140					

- (2) INFORMATION FOR SEQ ID NO:10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser 1 5 10 15

Gly Ala Tyr Gly Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu 20 25 30



PCT/US94/10308

WO 95/07301

Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser 35 40 45

Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly 50 . 55 60

Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Lys Arg
65 70 75 80

Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser 85 90 95

Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr 100 105 110

Ala Thr Tyr Tyr Cys Ala Arg Glu Thr Val Phe Tyr Trp Tyr Phe 115 120 125

Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser 130 135 140

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 423 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..423
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG GTG TTG CAG ACC CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT





WO 95/07301

		Leu	Gln	Thr	Gln	Val	Phe	Ile	Ser	Leu	Lev	Leu	Trp	·Ile	Ser	
1				5			•		10)				15		
GGT	GCC	TAC	GGG	CAG	GTT	ACC	CTG	CGT	GAA	TCC	GGI	CCG	GCA	CTA	GTT	96
Gly	Ala	Tyr	Gly	Gln	Val	Thr	Leu	Arg	Glu	Ser	Gly	Pro	Ala	Leu	Val	
			20					25					30			
AAA	CCG	ACC	CAG	ACC	CTG	ACG	TTA	ACC	TGC	ACC	TTC	TCC	·GGT	TTC	TCC	144
Lys	Pro	Thr	Gln	Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	Ser	Gly	Phe	Ser	
		35					40					45				
CTG	TCG	ACC	TCC	GGT	ATG	GGT	GTT	TCC	TGG	ATC	CGT	CAG	CCG	CCG	GGT	192
Leu	Ser	Thr	Ser	Gly	Met	Gly	Val	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	
	50					55					60					
AAA	GGT	CTA	GAA	TGG	CTG	GCT	CAC	ATC	TAC	TGG	GAC	GAC	GAC	AAA	CGT	240
Lys	Gly	Leu	Glu	Trp	Leu	Ala	His	Ile	Tyr	Trp	Asp	Asp	Asp	Lys	Arg	
65					70					75					80	
TAC	AAC	CCG	AGC	CTG	AAA	TCC	CGT	CTG	ACG	ATA	TCC	AAA	GAC	ACC	TCC	288
Tyr	Asn	Pro	Ser		Lys	Ser	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	
				85					90					95		
CGT	AAC	CAG	GTT	GTT	CTG	ACC	ATG	ACT	AAC	ATG	GAC	CCG	GTT	GAC	ACC	336
Arg	Asn	Gln		Val	Leu	Thr	Met	Thr	Asn	Met	Asp	Pro	Val	Asp	Thr	
			100					105					110			
GCT	ACC	TAC	TAC	TGC	GCT	CGA	CGC	GAA	ACC	GTT	TTC	TAC	TGG	TAC	TTC	384
Ala	Thr	Tyr	Tyr	Cys	Ala	Arg	Arg	Glu	Thr	Val	Phe	Tyr	Trp	Tyr	Phe	
		115					120					125	-	_		
SAC	GTT	TGG	GGT	CGT	GGT	ACC	CCA	GTT	ACC	GTG	AGC	TCA				423
							Pro									
	130					135					140					

(2) INFORMATION FOR SEQ ID NO:12:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
- Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser 1 5 10 15
- Gly Ala Tyr Gly Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val 20 25 30
- Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser 35 40 45
- Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly 50 55 60
- Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg 65 70 75 80
- Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser 85 90 95
- Arg Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr 100 105 110
- Ala Thr Tyr Tyr Cys Ala Arg Glu Thr Val Phe Tyr Trp Tyr Phe
 115 120 125
- Asp Val Trp Gly Arg Gly Thr Pro Val Thr Val Ser Ser 130 135 140
- (2) INFORMATION FOR SEQ ID NO:13:





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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: CDNA

(ix) FEATURE:

WO 95/07301

(A) NAME/KEY: CDS

(B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	48
															Gly	
1				5					10				•	15	-	
GTC	CAC	TCC	GAT	ATC	GTG	ATG	ACC	CAG	TCT	CCA	GAC	TCG	CTA	GCT	GTG	. 96
Val	His	Ser	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	
			20					25					. 30			
				•												
TCT	CTG	GGC	GAG	AGG	GCC	ACC	ATC	AAC	TGC	AAG	GCC	TCC	CAA	AGT	GTT	144
Ser	Leu	Gly	Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ala	Ser	Gln	Ser	Val	
		35					40		•			45				
GAT	TAT	GAT	ggt	GAT	AGT	TAT	ATG	AAC	TGG	TAT	CAG	CAG	AAA	ccc	GGG	192
Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	
	50					55					60					
													GAA			240
	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	
65					70					75					80	
								•								
													TTC			. 288
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	
				85					90					95		
													TAC			336
Thr	Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	



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110

CAA AGT AAT GAG GAT CCT CCG AGG TTC GGC GGA GGG ACC AAG GTG GAG

Gln Ser Asn Glu Asp Pro Pro Arg Phe Gly Gly Gly Thr Lys Val Glu

115

120

125

ATC AAA CGT Ile Lys Arg 130

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WO 95/07301

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(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: ·linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

Val His Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val 20 25 30

Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val 35 40 45

Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly 65 70 75 80

45

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu 85 90 95

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
100 105 110

Gln Ser Asn Glu Asp Pro Pro Arg Phe Gly Gly Gly Thr Lys Val Glu 115 120 125

Ile Lys Arg 130

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- (2) INFORMATION FOR SEQ ID NO:15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..45
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAG GCC AGC CAA AGT GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC
Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn

1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:16:
 - (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 15 amino acids

(B) TYPE: amino acid(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn

1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:17:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: CDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..21
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCT GCA TCC AAT CTA GAA TCT Ala Ala Ser Asn Leu Glu Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:18:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Ala Ser Asn Leu Glu Ser

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(2) INFORMATION FOR SEQ ID NO:19:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..27
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAG CAA AGT AAT GAG GAT CCT CCG ACG Gln Gln Ser Asn Glu Asp Pro Pro Thr

- (2) INFORMATION FOR SEQ ID NO:20:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein





21

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gin Gin Ser Asn Glu Asp Pro Pro Thr
1 5

- (2) INFORMATION FOR SEQ ID NO:21:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..21
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACT TCT GGT ATG GGT GTG AGC Thr Ser Gly Met Gly Val Ser

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- (2) INFORMATION FOR SEQ ID NO:22:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Thr Ser Gly Met Gly Val Ser

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(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..48

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAC ATT TAC TGG GAT GAT GAC AAG CGC TAT AAC CCA TCC CTG AAG AGC

His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser Leu Lys Ser

1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:24:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser Leu Lys Ser

1 5 10 15

(2) INFORMATION FOR SEQ ID NO:25:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGA GAG ACT GTG TTC TAC TGG TAC TTC GAT GTC
Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp Val
1 5 10

33

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein .

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp Val

- (2) INFORMATION FOR SEQ ID NO:27:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..27
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAG CAA AGT AAT GAG GAT CCT CCG AGG Gln Gln Ser Asn Glu Asp Pro Pro Arg

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- (2) INFORMATION FOR SEQ ID NO:28:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gin Gin Ser Asn Glu Asp Pro Pro Arg
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(2) INFORMATION FOR SEQ ID NO:29:





111	SECTIENCE	CHARACTERISTICS:
(_)	SECUENCE	CHARACTERISTICS

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTAACACTCA TTCCTGTTGA AGCTCTTGAC AATGGG

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- (2) INFORMATION FOR SEQ ID NO:30:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTACATATGC AAGGCTTACA ACCACAATC

- (2) INFORMATION FOR SEQ ID NO:31:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: DNA (genomic)



(xi)	SEQUENCE	DESCRIPTION:	SEO	ID	NO:	31	•
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GGTTACCCTG	CGTGAATCCG	GTCCGGCACT	AGTTAAACCG	ACCCAGACCC	TGACGTTAAC	60
CTGCACCTTC	TCCGGTTTCT	CCCTGTCGAC	CTCCGGTATG	GGTGTTTCCT	GGATCCG	117

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCAGCCGCCG GGTAAAGGTC TAGAATGGCT GGCTCACATC TACTGGGACG ACGACAAACG 60
TTACAACCCG AGCCTGAAAT CCCGTCTGAC GATATCCAAA GACACCTCCC GTAACCAGGT 120

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

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(ii) MOLECULE	TYPE:	DNA	(genomic)
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TGTTCTGACC ATGGACCCGG TTGACACCGC TACCTACTAC TGCGCTCGTC GCGAAACCGT 60

TTTCTACTGG TACTTCGACG TTTGGGGTCG TGGTACCCCA GTTACCGTGA GCTCCCAACC 120

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACCCGGCGGC TGACGGATCC AGGAA

25

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGGTCAGAA CAACCTGGTT ACGG

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs .

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCGGGTTAC CCTGCGTGAA TCCGG

25

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCAACCCTCG AGTGCCATTG A

21

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
CTAGCTGTGT CTCTGGGCGA GAGGGCCACC ATCAACTGCA AGG	43
(2) INFORMATION FOR SEQ ID NO:39:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 39 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: DNA (genomic)	·
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
CCTTGCAGTT GATGGTGGCC CTCTCGCCCA GAGACACAG	39
·	
(2) INFORMATION FOR SEQ ID NO:40:	
(i) Charles and a company of the com	
(i) SEQUENCE CHARACTERISTICS:	·
(A) LENGTH: 67 base pairs	•
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO.40.	

TCGAGAGGCC TCCCAAAGTG TTGATTATGA TGGTGATAGT TATATGAACT GGTATCAGCA

51



(2)	INFORMA?	TION FOR	SEQ	ID	NO:41:
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- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGGTTTCTGC TGATACCAGT TCATATAACT ATCACCATCA TAATCAACAC TTTGGGAGGC 60

CTC 63

- (2) INFORMATION FOR SEQ ID NO:42:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATACTACTGT CAGCAAAGTA ATGAGGATCC TCCGAGGTTC GGCGGAGGGA C

- (2) INFORMATION FOR SEQ ID NO:43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown



51

(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:	
CTTGGTCCCT CCGCCGAACC TCGGAGGATC CTCATTACTT TGCTGACAGT AGT	53
(2) INFORMATION FOR SEQ ID NO:44:	
(2) INFORMITON FOR SEQ ID NO:44:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 55 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:	
GGGCAGCCTC CTAAGTTGCT CATTTACGCT GCATCCAATC TAGAATCTGG GGTAC	. 55
(2) INFORMATION FOR SEQ ID NO:45:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 51 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: unknown	
(11) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:	

(2) INFORMATION FOR SEQ ID NO:46:

CCCAGATTCT AGATTGGATG CAGCGTAAAT GAGCAACTTA GGAGGCTGCC C

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(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 83 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: DNA (genomic)	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:46:	
AATTCGAGGA CGCCAGCAAC ATGGTGTTGC AGACCCAGGT CTTCATTTCT CTGTTGCTCT	60
GGATCTCTGG TGCCTACGGG CAG	8:
(2) INFORMATION FOR SEQ ID NO:47:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 84 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:	
GTAACCTGCC CGTAGGCACC AGAGATCCAG AGCAACAGAG AAATGAAGAC CTGGGTCTGC	60
AACACCATGT TGCTGGCGTC CTCG	84
(2) INFORMATION FOR SEQ ID NO:48:	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CAGGTTACCC TGAAAGAGTC

20

(2) INFORMATION FOR SEQ ID NO:49:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAAGTAGTCC TTGACCAG

18

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTCACCGTCT CCTCAGCTAG CACCAAGGGG C

31

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTTGGTGCTA GCTGAGGAGA CG

22

- (2) INFORMATION FOR SEQ ID NO:52:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CATCTAGATG GCGCCGCCAC AGTACGTTTG ATCTCCAGCT TGGTCCC

- (2) INFORMATION FOR SEQ ID NO:53:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: CDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:





AAGGCCTCCC AAAGTGTTGA TTATGATGGT GATAGTTATA TGAAC

45

- (2) INFORMATION FOR SEQ ID NO:54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACCTCCGGTA TGGGTGTTTC C

21

- (2) INFORMATION FOR SEQ ID NO:55:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CACATCTACT GGGACGACGA CAAACGTTAC AACCCGAGCC TGAAATCC

- (2) INFORMATION FOR SEQ ID NO:56:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs

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(B)	TYPE:	nuc	leic	acid
(C)	STRANI	DEDN	ESS:	double
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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGCGAAACCG TTTTCTACTG GTACTTCGAC GTT

33

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: CDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	48
Met	Gly	Trp	Ser	Суз	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
1				5					10					15	_	

GTC	CAC	TCC	GAT	ATC	GTG	ATG	ACC	CAG	TCT	CÇA	GAC	TCG	CTA	GCT	GTG	96
Val	His	Ser	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	
			20					25					30			

TCT	CTG	GGC	GAG	AGG	GCC	ACC	ATC	AAC	TGC	AAG	GCC	TCC	CAA	AGT	GTT	144
Ser	Leu	Gly	Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ala	Ser	Gln	Ser	Val	
		35					40					45				



GAT	TAT	Gat	GGT	GAT	AGT	TAT	ATG	AAC	TGG	TAT	CAG	CAG	AAA	ccc	GGG	192
Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	
	50					55					60					
CAG	CCT	CCT	AAG	TTG	CTC	ATT	TAC	GCT	GCA	TCC	AAT	CTA	GAA	TCT	GGG	240
Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	
65					70					75					80	
	CCT															288
Val	Pro	Asp	Arg		Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	•
				85					90		,			95		
	ATC															336
Thr	Ile	Ser		Leu	Gln	Ala	Glu		Val	Ala	Val	Tyr	Tyr	Cys	Gln	
			100				•	105					110			
C N N	3 C III	2 2 77	CNC	C 3 m												
	AGT															384
GIII	Ser	115	Gru	wah	PIO	PIO	120	Pne	GIĀ	GIĀ	GIY		Lys	Val	Glu	
		113					120					125				
ATC	AAA	CGT													,	393
	Lys			•				*							•	393
	130															

- (2) INFORMATION FOR SEQ ID NO:58:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

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WO 95/07301 PCT/US94/10308



Val	His	Ser	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val
			20					25					30		

- Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val
- Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
 50 55 60
- Gin Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly
 65 70 75 80
- Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu 85 90 95
- Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
 100 105 110
- Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu 115 120 125

Ile Lys Arg